

QY 541 KVTGTEVEIPVYHDPKGEAVLPSVFEDGTRQGMWAGSGVKTALTIBEANGSNALSWEF 600
 DB 541 KVTGTEVEIPVYHDPKGEAVLPSVFEDGTRQGMWAGSGVKTALTIBEANGSNALSWEF 600
 QY 601 GYEVKPSDNWMAFAPLDFWKSJDLVGENDYVAFDFTLDPVRATEGAMINLVFOPTNG 660
 DB 601 GYEVKPSDNWMAFAPLDFWKSJDLVGENDYVAFDFTLDPVRATEGAMINLVFOPTNG 660
 QY 661 YWVQAKRTYITINDELBEANQVNGLYHYEYKINVRDITNIQDITLLRNMMIIFADVESDF 720
 DB 661 YWVQAKRTYITINDELBEANQVNGLYHYEYKINVRDITNIQDITLLRNMMIIFADVESDF 720
 QY 721 AGRVFVDNVPFEGAAATTEPVEPVPDGEETPPVDEKAKGQKAEKEKEKE 773
 DB 721 AGRVFVDNVPFEGAAATTEPVEPVPDGEETPPVDEKAKGQKAEKEKEKE 773

RESULT 3

US-10-383-630-2
 Sequence 2, Application US/10383630
 Publication No. US20040002431A1
 GENERAL INFORMATION:
 APPLICANT: HAKUMADA, YOSHIMIRO
 APPLICANT: SAMADA, KAZUHISA
 APPLICANT: ENDO, KEIJI
 APPLICANT: KODAMA, HIROSHI
 APPLICANT: WADA, YASUNAO
 APPLICANT: SHIKATA, SHITSU
 APPLICANT: KOBAYASHI, TOHRU
 TITLE OF INVENTION: Mutant alkali cellulase
 FILE REFERENCE: 234890USO
 CURRENT APPLICATION NUMBER: US/10/383, 630
 CURRENT FILING DATE: 2003-03-10
 PRIOR APPLICATION NUMBER: JP P2002-089531
 PRIOR FILING DATE: 2002-03-27
 PRIOR APPLICATION NUMBER: JP P2003-013840
 PRIOR FILING DATE: 2003-01-22
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 824
 TYPE: PRT
 ORGANISM: Bacillus sp. KSM-S237
 US-10-383-630-2

Query Match 98.3%; Score 4059; DB 4; Length 824;
 Best Local Similarity 98.2%; Pred. No. 8.8e-293;
 Matches 758; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 AEGNTREDNFHLLGNDNVKRPSEAGALQLOEVGQMTLVDOHGEKIQLRGMSHTGLQMF 60
 DB 30 AEGNTREDNFHLLGNDNVKRPSEAGALQLOEVGQMTLVDOHGEKIQLRGMSHTGLQMF 89
 QY 61 PEIINDNAYKALANDMESNMIRLAMYGENGYASNPILKSRVYKGIIDALENDMYIVD 120
 DB 90 PEIINDNAYKALANDMESNMIRLAMYGENGYASNPILKSRVYKGIIDALENDMYIVD 149
 QY 121 WHVAPGDPBPVYAGADPFREIDTALYPNNPHIYELANPSSNNNGAGIPNNBEGMN 180
 DB 150 WHVAPGDPBPVYAGADPFREIDTALYPNNPHIYELANPSSNNNGAGIPNNBEGMN 209
 QY 181 AVKEVADPIVEMLRDSGNADNIIIVGSPNNQSQRDLADNPINDHMTYVHFYTGSHA 240
 DB 210 AVKEVADPIVEMLRDSGNADNIIIVGSPNNQSQRDLADNPINDHMTYVHFYTGSHA 269
 QY 241 ASTESYPTPTNSERGNVSNTRYALENGVAFATEMGTSQANGCGGYFDEADYWEFL 300
 DB 270 ASTESYPTPTNSERGNVSNTRYALENGVAFATEMGTSQANGCGGYFDEADYWEFL 329
 QY 301 NNNNSIWNWSLTNGEVSAGFTPELIGKSNATNIDPGPDHMADEEELSLGEYVRAIK 360
 DB 330 NNNNSIWNWSLTNGEVSAGFTPELIGKSNATNIDPGPDHMADEEELSLGEYVRAIK 389

QY 361 GNVYEBIDRTKTKYLMDFENDGTQGFVNSDSPNKELIADVNNNTLVSGLDVSNDS 420
 DB 390 GNVYEBIDRTKTKYLMDFENDGTQGFVNSDSPNKELIADVNNNTLVSGLDVSNDS 449
 QY 421 DGNFMANRLSADGKGSVDIIGAEKLTMDVYDEBTTVAIAIIPQSSKSGANPERAAR 480
 DB 450 DGNFMANRLSADGKGSVDIIGAEKLTMDVYDEBTTVAIAIIPQSSKSGANPERAAR 509
 QY 481 VNAEDPVQOTDGYKAGLTITGEDAPNLKNIAPHEEDNNNNIILFVGTDAADVILDN 540
 DB 510 VNAEDPVQOTDGYKAGLTITGEDAPNLKNIAPHEEDNNNNIILFVGTDAADVILDN 569
 QY 541 KVTGTEVEIPVYHDPKGEAVLPSVFEDGTRQGMWAGSGVKTALTIBEANGSNALSWEF 600
 DB 541 KVTGTEVEIPVYHDPKGEAVLPSVFEDGTRQGMWAGSGVKTALTIBEANGSNALSWEF 629
 QY 601 GYEVKPSDNWMAFAPLDFWKSJDLVGENDYVAFDFTLDPVRATEGAMINLVFOPTNG 660
 DB 630 GYEVKPSDNWMAFAPLDFWKSJDLVGENDYVAFDFTLDPVRATEGAMINLVFOPTNG 689
 QY 661 YWVQAKRTYITINDELBEANQVNGLYHYEYKINVRDITNIQDITLLRNMMIIFADVESDF 720
 DB 690 YWVQAKRTYITINDELBEANQVNGLYHYEYKINVRDITNIQDITLLRNMMIIFADVESDF 749
 QY 721 AGRVFVDNVPFEGAAATTEPVEPVPDGEETPPVDEKAKGQKAEKEKEKE 772
 DB 750 AGRVFVDNVPFEGAAATTEPVEPVPDGEETPPVDEKAKGQKAEKEKEKE 801

RESULT 4

US-10-479-214-2
 Sequence 2, Application US/10479214
 Publication No. US2004024829A1
 GENERAL INFORMATION:
 APPLICANT: KAO CORPORATION
 APPLICANT: Sawada, Kazuhisa
 APPLICANT: Ozaki, Katsuya
 APPLICANT: Tohata, Masatoshi
 APPLICANT: Ozawa, Tadahiro
 APPLICANT: Endo, Keiji
 TITLE OF INVENTION: HOST MICROORGANISMS
 FILE REFERENCE: 244691US-0-PCT
 CURRENT APPLICATION NUMBER: US/10/479, 214
 CURRENT FILING DATE: 2003-12-01
 PRIOR APPLICATION NUMBER: PCT/JP02/05151
 PRIOR FILING DATE: 2002-05-28
 PRIOR APPLICATION NUMBER: Japan 2001-160920
 PRIOR FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2
 LENGTH: 824
 TYPE: PRT
 ORGANISM: Bacillus sp. KSM-S237
 US-10-479-214-2

Query Match 98.3%; Score 4059; DB 5; Length 824;
 Best Local Similarity 98.2%; Pred. No. 8.8e-293;
 Matches 758; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 AEGNTREDNFHLLGNDNVKRPSEAGALQLOEVGQMTLVDOHGEKIQLRGMSHTGLQMF 60
 DB 30 AEGNTREDNFHLLGNDNVKRPSEAGALQLOEVGQMTLVDOHGEKIQLRGMSHTGLQMF 89
 QY 61 PEIINDNAYKALANDMESNMIRLAMYGENGYASNPILKSRVYKGIIDALENDMYIVD 120
 DB 90 PEIINDNAYKALANDMESNMIRLAMYGENGYASNPILKSRVYKGIIDALENDMYIVD 149
 QY 121 WHVAPGDPBPVYAGADPFREIDTALYPNNPHIYELANPSSNNNGAGIPNNBEGMN 180
 DB 150 WHVAPGDPBPVYAGADPFREIDTALYPNNPHIYELANPSSNNNGAGIPNNBEGMN 209
 QY 181 AVKEVADPIVEMLRDSGNADNIIIVGSPNNQSQRDLADNPINDHMTYVHFYTGSHA 240